

8. (Three Times Amended) A primer for amplifying a nucleotide sequence, said primer having at least 85% homology with a fragment of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein said primer contains at least 5 and no more than 30 nucleotides.

11. (Twice Amended) A reagent for detecting or identifying *Trypanosoma cruzi* in a biological sample, said reagent comprising a capture probe and a detection probe, both in accordance with claim 5, wherein said capture probe and said detection probe have nucleotide sequences that are different from one another.

18. (Amended) A method for detection and/or identification of *Trypanosoma cruzi* in a biological sample, comprising exposing denatured DNA extracted from *Trypanosoma cruzi* or DNA obtained by reverse transcription of RNA extracted from *Trypanosoma cruzi* to at least one probe according to claim 5; and detecting hybridization of said probe.

21. (Twice Amended) A synthetic or isolated nucleic acid fragment that comprises a nucleotide sequence having at least 85% homology with a reference sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein each segment of 30 contiguous nucleotides of said nucleotide sequence has at least 85% homology with a segment of 30 contiguous nucleotides of said reference sequence.

22. (Twice Amended) The nucleic acid fragment of claim 21, said nucleotide sequence having at least 85% homology with a second reference sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein each segment of 30 contiguous nucleotides of said nucleotide sequence has at least 85% homology with a segment of 30 contiguous nucleotides of said second reference sequence.

23. (Twice Amended) A synthetic or isolated nucleic acid fragment that comprises a nucleotide sequence having at least 85% homology with a reference sequence that is identical or fully complementary to a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein each segment of 30 contiguous nucleotides of said nucleotide sequence has at least 85% homology with a segment of 30 contiguous nucleotides of said reference sequence.

24. (Twice Amended) The nucleic acid fragment of claim 23, wherein said nucleotide sequence is identical or fully complementary to a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence.

32. (Amended) The reagent of claim 17, wherein said primer contains no more than 30 nucleotides.

34. (Amended) The method of claim 20, wherein said primer contains no more than 30 nucleotides.

Please add new claims 36-40 as follows:

--36. The nucleic acid fragment of claim 21, wherein said nucleotide sequence (a) is a nucleic acid sequence that is identical to or is a degenerate of a sequence starting at nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence, or (b) is a full complement of said nucleic acid sequence.--

--37. The nucleic acid fragment of claim 22, wherein said nucleotide sequence (a) is a nucleic acid sequence that is identical to or is a degenerate of a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, or (b) is a full complement of said nucleic acid sequence.--

--38. The nucleic acid fragment of claim 23, wherein said nucleotide sequence (a) is a nucleic acid sequence that is identical to or is a degenerate of a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, or (b) is a full complement of said nucleic acid sequence.--